

AMENDMENTS TO THE CLAIMS

1. – 16. (Canceled)

17. (New) A method for improving thermostability of proteins, which comprises:

(i) comparing amino acid sequences of proteins belonging to the same family and deriving from two or more species, wherein said proteins evolutionarily correspond to each other in a phylogenetic tree;

(ii) estimating an amino acid sequence of an ancestral protein corresponding to the amino acid sequences of the proteins in (i);

(iii) comparing the amino acid residues in the amino acid sequence in one of the proteins compared in (i) with amino acid residues at a corresponding position in the ancestral protein estimated in (ii), and replacing one or more amino acid residues of the protein different from those of the ancestral protein with the same amino acid residues as those of the ancestral protein;

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B (iv) testing the proteins obtained in (iii) for thermostability; and

(v) selecting a protein having improved thermostability.

18. (New) The method for improving thermostability of protein according to claim 17, wherein thermophilic bacteria or archaebacteria are included in the species from which the protein to be compared is derived in (i).

19. (New) The method of claim 17, wherein the protein being tested for improved thermostability is a 3-isopropylmalate dehydrogenase.

20. (New) The method of claim 17, wherein the protein being tested for improved thermostability is an isocitrate dehydrogenase.

21. (New) The method of claim 17, wherein said estimating is by the maximum parsimony method.

22. (New) The method of claim 17, wherein said estimating is by the neighbor joining method.

23. (New) A method for improving thermostability of proteins, which comprises

(i) comparing amino acid sequences of proteins belonging to the same family and deriving from two or more species, wherein said proteins evolutionarily correspond to each other in a phylogenetic tree by multiple alignment;

(ii) estimating an amino acid sequence of an ancestral protein corresponding to the amino acid sequences of the proteins in (i);

(iii) comparing the amino acid residues in the amino acid sequence in one of the proteins compared in (i) with amino acid residues at a corresponding position in the ancestral protein estimated in (ii), and replacing one or more amino acid residues of the protein different from those of the ancestral protein with the same amino acid residues as those of the ancestral protein;

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----- (iv) testing the proteins obtained in (iii) for thermostability; and -----

(v) selecting a protein having improved thermostability.

24. (New) The method for improving thermostability of protein according to claim 23, wherein thermophilic bacteria or archaebacteria are included in the species from which the protein to be compared is derived in (i).

25. (New) The method of claim 23, wherein said estimating is by the maximum parsimony method.

26. (New) The method of claim 23, wherein said estimating is by the neighbor joining method.

SUPPORT FOR THE AMENDMENT

Claims 1-16 have been canceled.

Claims 17-26 have been added.

New Claims 17-26 are supported by Claims 1-16 as originally filed. The specification has also been amended to correct minor typographical and grammatical errors. Support for these amendments can be found in the specification and drawings as originally filed.

No new matter is believed to have been entered by the present amendment.